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<141> 2001-08-22  
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tcatggacca cgcccaagca cacgaccta tcaggtattc gttgcaaacc atacatcgat 180  
gatagatttc attattctgg agcaaatgac agcatttgct gtcatcatgc agaagcatcc 240  
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ccaaacaca ctgaagagaa acaacgcata tttgccaat ctgtcttgat gagactggag 780  
gagaaatgaa gggacgtaaa gccgtacaag tgcacttcgt tagggttta catgcagcta 840  
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<212> PRT  
<213> Zea mays

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 Ser Trp Thr Gly Val Ile Lys Tyr His Gly Pro Arg Pro Ser Thr Arg  
 35 40 45  
 Pro His Gln Val Phe Val Ala Asn His Thr Ser Met Ile Asp Phe Ile  
 50 55 60  
 Ile Leu Glu Gln Met Thr Ala Phe Ala Val Ile Met Gln Lys His Pro  
 65 70 75 80  
 Gly Trp Val Gly Phe Ile Gln Lys Thr Ile Leu Glu Ser Val Gly Cys  
 85 90 95  
 Ile Trp Phe Asn Arg Asn Asp Leu Arg Asp Arg Glu Val Thr Ala Arg  
 100 105 110  
 Lys Leu Arg Asp His Val Gln Gln Pro Asp Asn Asn Pro Leu Leu Ile  
 115 120 125  
 Phe Pro Glu Gly Thr Cys Val Asn Asn Gln Tyr Thr Val Met Phe Lys  
 130 135 140  
 Lys Gly Ala Phe Glu Leu Gly Cys Ala Val Cys Pro Ile Ala Ile Lys  
 145 150 155 160  
 Tyr Asn Lys Ile Phe Val Asp Ala Phe Trp Asn Ser Lys Lys Gln Ser  
 165 170 175  
 Phe Thr Met His Leu Val Arg Leu Met Thr Ser Trp Ala Val Val Cys  
 180 185 190  
 Asp Val Trp Tyr Leu Pro Pro Gln Tyr Leu Arg Glu Gly Glu Thr Ala  
 195 200 205  
 Ile Ala Phe Ala Glu Arg Val Arg Asp Met Ile Ala Ala Arg Ala Gly  
 210 215 220  
 Leu Lys Lys Val Pro Trp Asp Gly Tyr Leu Lys His Asn Arg Pro Ser  
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aatcattact gaaaaagtaa ananatatac attattttc ctcaaagcgc cgcaacacag 180  
actcancgaa tatttgttgc ttcccttctc tgtgcttggg actaggcgaa gaatacttca 240  
natancatc ccaaggaacc ttttaagcc cagcacgatg tgagattatg tctctaactc 300  
tctctgcaaa ttcaatgggt gtctctcctg gcttcaaatt ttgtggntcc aagtaccata 360  
catcacannn nacagcccaa gatgtcatta attgcaagag atgnctggtg aangattgct 420  
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<213> Glycine max

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Trp Ala Val Xaa Cys Asp Val Trp Tyr Leu Xaa Pro Gln Asn Leu Lys  
35 40 45

Pro Gly Glu Thr Pro Ile Glu Phe Ala Glu Arg Val Arg Asp Ile Ile  
50 55 60

Ser His Arg Ala Gly Leu Lys Val Pro Trp Asp Gly Tyr Xaa Lys  
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Tyr Ser Arg Pro Ser Pro Lys His Arg Glu Gly Lys Gln Gln Ile Phe  
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Xaa Glu Ser Val Leu Arg Arg Phe Glu Glu Lys  
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ggaaaagtgtg gttgcacatcg ggttaaccg taatgatctc aaggatcgtg aagttagttgg 240
aagaaaagtta cgtgatcaag ttcagcatcc agacaacaat cctctcttga ttttcccgaa 300
aggaacttgtt gttaataatc agtacactgt gatgttcaag aagggtgctt ttgagcttgg 360
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<213> Triticum aestivum

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Ile Ile Leu Glu Gln Met Thr Ala Phe Ala Val Ile Met Gln Lys His  
35 40 45

Pro Gly Trp Val Gly Phe Ile Gln Lys Thr Ile Leu Glu Ser Val Val  
50 55 60

Ala Ser Gly Phe Asn Arg Asn Asp Leu Lys Asp Arg Glu Val Val Gly  
65 70 75 80

Arg Lys Leu Arg Asp Gln Val Gln His Pro Asp Asn Asn Pro Leu Leu  
85 90 95

Ile Phe Pro Glu Gly Thr Cys Val Asn Asn Gln Tyr Thr Val Met Phe  
100 105 110

Lys Lys Gly Ala Phe Glu Leu Gly Cys Ala Val Cys Pro Ile Ala Ile  
115 120 125

Lys Tyr Asn Lys Ile Phe Val Asp Ala Phe Trp Asn Ser Lys Lys Gln  
130 135 140

Ser Phe Thr Met His Leu Val Arg Leu Met Thr Ser Trp Ala Val Val  
145 150 155 160

Cys Asp Val Trp Ser Trp Glu Pro Gln Tyr Leu Arg Glu Gly Glu Thr  
165 170 175

Ala Ile Glu Phe Thr Glu Arg Val Arg Asp Met Ile Ala Ala Arg Ala  
180 185 190

Gly Leu Lys Lys Val Pro Trp Asp Gly Tyr Leu Lys His Asn Arg Pro  
195 200 205

Ser Pro Lys His Thr Glu Glu Lys Gln Arg Met Phe Ala Glu Ser Val  
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Leu Arg Arg Leu Glu Glu Asn  
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<212> DNA

<213> Zea mays

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cgaagtcttc agaagctaaa ggtgtctcag gcgctgtaac tgaaaggatc caagacgttt 420

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tgctgtttt	tatacctgta	atgtggcagt	ttatttgtt	gaggaggctg	ttgagtaccc	960
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<212> PRT

<213> Zea mays

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Arg	Val	Met	Leu	Phe	Val	Phe	Gly	Phe	Tyr	Trp	Ile	Arg	Glu	Thr	Arg
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Arg	Arg	Ser	Thr	Asn	Ala	Lys	Gly	Leu	Asn	Gln	Asp	Gln	Phe	Glu	Glu
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Ser	Gln	Arg	Pro	Gly	Ala	Ile	Val	Ser	Asn	His	Val	Ser	Tyr	Val	Asp
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Ile	Leu	Tyr	His	Met	Ser	Ala	Ser	Phe	Pro	Ser	Phe	Val	Ala	Lys	Glu
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Ser	Val	Ser	Arg	Leu	Pro	Leu	Ile	Gly	Leu	Ile	Ser	Asn	Cys	Leu	Gly
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Cys	Ile	Phe	Val	Gln	Arg	Glu	Ser	Lys	Ser	Ser	Glu	Ala	Lys	Gly	Val
					115			120			125				

Ser	Gly	Ala	Val	Thr	Glu	Arg	Ile	Gln	Asp	Val	Cys	Gln	Asp	Lys	Asn
					130		135			140					

Thr	Pro	Met	Met	Leu	Leu	Phe	Pro	Glu	Gly	Thr	Thr	Asn	Gly	Asp	
					145		150			155			160		

Tyr	Leu	Leu	Pro	Phe	Lys	Thr	Gly	Ala	Phe	Leu	Ala	Gly	Ala	Pro	Val
					165			170			175				

Gln	Pro	Val	Ile	Leu	Lys	Tyr	Pro	Tyr	Arg	Arg	Phe	Ser	Pro	Ala	Trp
					180			185			190				

Asp	Ser	Met	Asp	Gly	Ala	Arg	His	Val	Phe	Leu	Leu	Cys	Gln	Phe	
					195			200			205				

Val	Asn	His	Met	Glu	Val	Val	Arg	Leu	Pro	Val	Tyr	Tyr	Pro	Ser	Gln
					210			215			220				

Leu Glu Lys Glu Asp Pro Lys Leu Tyr Ala Asn Asn Val Arg Lys Leu  
225 230 235 240

Ile Ala Met Glu Gly Asn Leu Val Leu Ser Asn Ile Gly Leu Ala Glu  
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Lys Arg Val Tyr His Ala Ala Leu Thr Gly Ser Ser Leu Pro Gly Ala  
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Arg His Glu Lys Asp Asp  
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<212> DNA

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35 40 45

Val Arg Arg Asp Val Tyr Gly Thr Met Gly Arg Gly Glu Leu Pro Pro  
50 55 60

Lys Glu Lys Leu Leu Leu Gly Phe Ala Leu Val Thr Leu Leu Pro Ile  
 65 70 75 80  
 Arg Val Val Leu Ala Val Thr Ile Leu Leu Phe Tyr Tyr Leu Ile Cys  
 85 90 95  
 Arg Val Cys Thr Leu Phe Ser Ala Pro Thr Gly Glu Glu Gln Glu  
 100 105 110  
 Asp Tyr Ala His Met Ser Gly Trp Arg Arg Thr Ile Ile Val Ser Cys  
 115 120 125  
 Gly Arg Ala Leu Ser Arg Leu Met Leu Phe Ile Phe Gly Phe Tyr Trp  
 130 135 140  
 Ile Pro Glu Ser Asn Ser Ala Ser Gln Glu Asp Lys Ser Arg Gln Pro  
 145 150 155 160  
 Glu Glu Leu Arg Arg Pro Gly Val Ile Ile Ser Asn His Val Ser Tyr  
 165 170 175  
 Leu Asp Ile Leu Tyr His Met Ser Ser Phe Pro Ser Phe Val Ala  
 180 185 190  
 Lys Arg Ser Val Ala Lys Leu Pro Leu Val Gly Leu Ile Ser Lys Cys  
 195 200 205  
 Leu Gly Cys Val Tyr Val Gln Arg Glu Ser Arg Ser Ser Asp Phe Lys  
 210 215 220  
 Gly Val Ser Ala Val Val Thr Asp Arg Ile Arg Glu Ala His Gln Asn  
 225 230 235 240  
 Glu Ser Ala Pro Leu Met Met Leu Phe Pro Glu Gly Thr Thr Asn  
 245 250 255  
 Gly Glu Phe Leu Leu Pro Phe Lys Thr Gly Gly Phe Leu Ala Lys Ala  
 260 265 270  
 Pro Val Leu Pro Val Ile Leu Arg Tyr His Tyr Gln Arg Phe Ser Pro  
 275 280 285  
 Ala Trp Asp Ser Ile Ser Gly Val Arg His Val Ile Phe Leu Leu Cys  
 290 295 300  
 Gln Phe Val Asn Tyr Met Glu Val Ile Arg Leu Pro Val Tyr His Pro  
 305 310 315 320  
 Ser Gln Gln Glu Met Asp Asp Pro Lys Leu Tyr Ala Asn Asn Val Arg  
 325 330 335  
 Arg Leu Met Ala Thr Glu Gly Asn Leu Ile Leu Ser Asp Ile Gly Leu  
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tcatatgtgg acattcttta tcataatgtca gcttcttctc cgagtttgt tgctaagaac 240
tcagtgtcca agttgccgtt gattggtctc ataagcaaat gtcttggtg cattttgtt 300
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      20          25          30

Arg Ser Phe Pro Asn Ala Glu Asp Val Pro Lys Asp His Tyr Glu Glu
      35          40          45

Leu Glu Arg Pro Gly Ala Ile Val Ser Asn His Val Ser Tyr Val Asp
      50          55          60

Ile Leu Tyr His Met Ser Ala Ser Ser Pro Ser Phe Val Ala Lys Asn
      65          70          75          80

Ser Val Ser Lys Leu Pro Leu Ile Gly Leu Ile Ser Lys Cys Leu Gly
      85          90          95

Cys Ile Phe Val Gln Arg Glu Pro Asn Val Gln Ile Leu Lys Gly Leu
     100         105         110

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Lys Cys Cys Asn Lys Ser Met Xaa Ser Gln Gly Arg Glu Ser Leu Tyr  
115 120 125

Leu Xaa Phe Pro Glu Xaa Thr Leu Gln Trp Asp Tyr Ser Pro Leu Xaa  
130 135 140

Arg Xaa Ser Cys Xaa Asp Met Gln Leu Tyr Leu Xaa Tyr Leu Gln Arg  
145 150 155 160

Leu Ser Thr Trp Asp His Asp Gly Thr Gln Val Phe Ala Pro Xaa Phe  
165 170 175

Xaa Xaa Xaa Arg Val Pro Ser Glu Xaa Leu Xaa Lys Arg Xaa Ser Ile  
180 185 190

Ser Lys

<210> 13

<211> 1501

<212> DNA

<213> Arabidopsis thaliana

<400> 13

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aaatcatgtt tcttatattg aaccaatctt ctacttctat gaattatcac cgaccattgt 180  
tgcacatcgag tcacatgatt cacttccatt tggttggact attatcaggg caatgcaggt 240  
gatatatgtg aatagattct cacagacatc aaggaagaat gctgtgcattg aaataaagag 300  
aaaagcttcc tgcgatagat ttccctcgct gctgttattc cccgaaggaa ccacgactaa 360  
tgggaaagtt cttatttcct tccaactcgg tgcttcatc cctggttacc ctattcaacc 420  
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gacgctcatg ttttagaatgt tcactcagtt tcacaatttc atggaggttg aatatcttcc 540  
tgtaatctat cccagtgaaa agcaaaagca gaatgctgtg cgtctctcac agaagactag 600  
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<211> 403

<212> PRT

<213> Arabidopsis thaliana

<400> 14

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Glu Ile Ala Pro Ile Val Val Ser Asn His Val Ser Tyr Ile Glu Pro  
                  35                     40                     45

Ile Phe Tyr Phe Tyr Glu Leu Ser Pro Thr Ile Val Ala Ser Glu Ser  
                  50                     55                     60

His Asp Ser Leu Pro Phe Val Gly Thr Ile Ile Arg Ala Met Gln Val  
                  65                     70                     75                     80

Ile Tyr Val Asn Arg Phe Ser Gln Thr Ser Arg Lys Asn Ala Val His  
                  85                     90                     95

Glu Ile Lys Arg Lys Ala Ser Cys Asp Arg Phe Pro Arg Leu Leu Leu  
                  100                    105                     110

Phe Pro Glu Gly Thr Thr Asn Gly Lys Val Leu Ile Ser Phe Gln  
                  115                    120                     125

Leu Gly Ala Phe Ile Pro Gly Tyr Pro Ile Gln Pro Val Val Val Arg  
                  130                    135                     140

Tyr Pro His Val His Phe Asp Gln Ser Trp Gly Asn Ile Ser Leu Leu  
                  145                    150                     155                     160

Thr Leu Met Phe Arg Met Phe Thr Gln Phe His Asn Phe Met Glu Val  
                  165                    170                     175

Glu Tyr Leu Pro Val Ile Tyr Pro Ser Glu Lys Gln Lys Gln Asn Ala  
                  180                    185                     190

Val Arg Leu Ser Gln Lys Thr Ser His Ala Ile Ala Thr Ser Leu Asn  
                  195                    200                     205

Val Val Gln Thr Ser His Ser Phe Ala Asp Leu Met Leu Leu Asn Lys  
                  210                    215                     220

Ala Thr Glu Leu Lys Leu Glu Asn Pro Ser Asn Tyr Met Val Glu Met  
                  225                    230                     235                     240

Ala Arg Val Glu Ser Leu Phe His Val Ser Ser Leu Glu Ala Thr Arg  
                  245                    250                     255

Phe Leu Asp Thr Phe Val Ser Met Ile Pro Asp Ser Ser Gly Arg Val  
                  260                    265                     270

Arg Leu His Asp Phe Leu Arg Gly Leu Lys Leu Lys Pro Cys Pro Leu  
                  275                    280                     285

Ser Lys Arg Ile Phe Glu Phe Ile Asp Val Glu Lys Val Gly Ser Ile  
                  290                    295                     300

Thr Phe Lys Gln Phe Leu Phe Ala Ser Gly His Val Leu Thr Gln Pro  
                  305                    310                     315                     320

Leu Phe Lys Gln Thr Cys Glu Leu Ala Phe Ser His Cys Asp Ala Asp  
                  325                    330                     335

Gly Asp Gly Tyr Ile Thr Ile Gln Glu Leu Gly Glu Ala Leu Lys Asn  
340 345 350

Thr Ile Pro Asn Leu Asn Lys Asp Glu Ile Arg Gly Met Tyr His Leu  
355 360 365

Leu Asp Asp Asp Gln Asp Gln Arg Ile Ser Gln Asn Asp Leu Leu Ser  
370 375 380

Cys Leu Arg Arg Asn Pro Leu Leu Ile Ala Ile Phe Ala Pro Asp Leu  
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Ala Pro Thr

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<211> 692

<212> DNA

<213> Oryza sativa

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<222> (579)

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<220>

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<222> (677)

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gccacgcggg gcaccataac cacgacgacg acgacgagga gtcgccaacg gtgtgcggcg 180  
gcgatggcgg aggagggggg gacccgttgc cgttcctatc ggaggatcgg ccggcgtgg 240  
ggtcgcccgg ggggtgtcc ccggccgacc cggtccgcaa cgggacgccc gggtggtgcg 300  
gggcgtacga gctcgtgagg gcgctcgtgt gcgccgggt ggcggcggcg aggctggtgc 360  
tgttcgggct ctccatcgcg gtggggtacg ccgccacgtg ggtggcgctc cgccgggtgg 420  
tcgacgtgcg ggagcggcg ggcgcggagg ggcgcgggcc catgcggcg tggcgccgccc 480  
gcctcatgtg gatcacgcgg attccgcgcg ctgcacatctc ttctccttcg gatacattgg 540  
ataaggagaa agaaaaacgg ccctagaaac ttcactatnt ttctaaatca tggtcatcat 600  
agaaccatat actctcatag ctccgacat cgttctcaaa tccatatcat acattttgaa 660  
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<213> Oryza sativa

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 Ser Asp Ser Ile Ser Pro Thr Pro Thr Thr Asn Gly His Ala Gly His  
   20               25   30  
  
 His Asn His Asp Asp Asp Glu Glu Ser Pro Thr Val Cys Gly Gly  
   35               40   45  
  
 Asp Gly Gly Gly Gly Asp Pro Phe Ala Phe Leu Ser Glu Asp Arg  
   50               55   60  
  
 Pro Ala Trp Trp Ser Pro Arg Gly Val Ser Pro Ala Asp Pro Phe Arg  
   65               70   75                           80  
  
 Asn Gly Thr Pro Gly Trp Cys Gly Ala Tyr Glu Leu Val Arg Ala Leu  
   85               90   95  
  
 Val Cys Ala Pro Val Ala Ala Ala Arg Leu Val Leu Phe Gly Leu Ser  
   100              105   110  
  
 Ile Ala Val Gly Tyr Ala Ala Thr Trp Val Ala Leu Arg Gly Trp Val  
   115              120   125  
  
 Asp Val Arg Glu Arg Ala Ala Xaa Glu Gly Ala Gly Pro Met Pro Ala  
   130              135   140  
  
 Trp Arg Arg Arg Leu Met Trp Ile Thr Arg Ile Pro Arg Ala Ala Ser  
   145              150   155                           160  
  
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cgctgcggct cgcgctgttc gggctctgcc tcgcgggtggg gtacgtggcg acgaagggtgg 180
cgctggcang gtggnaggac aaggagaatc ccatgccccaa gtggaggtgt agggttatgt 240
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ggatcacgcg cttgtgcgcc aaatgtattc tcttctcctt tggntatcan tggataaaac 300  
ggnaaggaa acctgcacca aggggaaatt gctccaataa attgtatcta aaccatgttt 360  
cntaanagtg agcctannct tcctatttct aagaattant tcctaacaat ggtgggaanc 420  
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Arg Asn Arg Thr Pro Ala Ile Glu Gly Leu Tyr Glu Trp Ala Lys Thr  
20 25 30

Ala Leu Cys Leu Pro Leu Ala Ala Leu Arg Leu Ala Leu Phe Gly Leu  
35 40 45

Cys Leu Ala Val Gly Tyr Val Ala Thr Lys Val Ala Leu Ala Xaa Trp  
50 55 60

Xaa Asp Lys Glu Asn Pro Met Pro Lys Trp Arg Cys Arg Val Met Trp  
65 70 75 80

Ile Thr Arg Leu Cys Ala Lys Cys Ile Leu Phe Ser Phe Gly Tyr Xaa  
85 90 95

Trp Ile Lys Arg Xaa Gly Lys Pro Ala Pro Arg  
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catctcgcc cccgagatt ggaagtgggg gcagggcagg gcggcagggg ccatggcggt 180
cccactcgatc ctgcgtgc tcccgctcg tccctcttc ctcctctccg gcctcaacgc 240
catccaggcc gtcctgttc tctcgataag gccgttctcg aagagcttgt accggcggat 300
caacaggttc ttggccgagc tgctgtggct tcagctggc tggcttgtgg attgggtggc 360
aggagttaaat atacaactgc atgctgatga cgaaaactaac aaggcaatgg ggaatgagca 420
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cacagcgctc aaggatgcct tggaagttac acttgctgtt atgaagaaac atccgaaatc 540
cttccaatta ttgggctggn ccatgttgc tgcagaatac cccttttgg gaaaaggact 600
ggccaaagga tgaaaagaca ttgaaatggg ggcccccaaa ggttgaanga cttccccaga 660
catttggcn acccttttg tttaaggacc cccttaccca acaaaactcc aacaactcaa 720
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Leu Leu Ser Gly Leu Asn Ala Ile Gln Ala Val Leu Phe Leu Ser Ile
      20          25          30

Arg Pro Phe Ser Lys Ser Leu Tyr Arg Arg Ile Asn Arg Phe Leu Ala
      35          40          45

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Glu Leu Leu Trp Leu Gln Leu Val Trp Leu Val Asp Trp Trp Ala Gly  
50 55 60

Val Lys Ile Gln Leu His Ala Asp Asp Glu Thr Tyr Lys Ala Met Gly  
65 70 75 80

Asn Glu His Ala Leu Val Ile Ser Asn His Arg Ser Asp Ile Asp Trp  
85 90 95

Leu Ile Gly Trp Ile Leu Gly Thr Ala Leu Lys Asp Ala Leu Gly Ser  
100 105 110

Thr Leu Ala Val Met Lys Lys His Pro Lys Ser Phe Gln Leu Leu Gly  
115 120 125

Trp Xaa Met Leu Phe Ala Glu Tyr Pro Phe Leu Gly Lys Gly Leu Gly  
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Lys Gly  
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ttgcagcagc ggccgtggtg gtaccattgg gcctgctttt ctgcgcctcc ggcctccctg 180  
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gaaggatcaa ccgggttagta gcagagctct tgtggctgga gcttgtatgg cttattgatt 300  
ggtgggcagg agttaaggc caaatattca cagatcatga aaccttcgt ttaatggta 360  
aagagcatgc acttgtgata agcaatcaca gaagtgatat tgattggctt gttggatggg 420  
tttcagctca gcgttcaggt tgtcttggca gcactctaag ctgtgatgaa gaaatctca 480  
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aantnngcc aaagatgaaa gcccattaaa gtcangcatc ccgg 584

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<211> 116  
<212> PRT  
<213> Glycine max

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Phe Ala Ser Gly Leu Leu Val Asn Leu Ile Gln Ala Ile Cys Tyr Val  
20 25 30

Val Val Arg Pro Val Ser Lys Ser Leu Tyr Arg Arg Ile Asn Arg Val  
35 40 45

Val Ala Glu Leu Leu Trp Leu Glu Leu Val Trp Leu Ile Asp Trp Trp  
50 55 60

Ala Gly Val Lys Val Gln Ile Phe Thr Asp His Glu Thr Phe Arg Leu  
65 70 75 80

Met Gly Lys Glu His Ala Leu Val Ile Ser Asn His Arg Ser Asp Ile  
85 90 95

Asp Trp Leu Val Gly Trp Val Ser Ala Gln Arg Ser Gly Cys Leu Gly  
100 105 110

Ser Thr Leu Ser  
115

<210> 23  
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cgcaatacgatc ataatgaaga aatcctcaaa gttccttcca gttattggtt ggtccatgtg 420  
gtttgcagaa tactctttt gagagaactg gcaaaggatg aaaaacacta aatcgggtct 480  
caaggtgaaa actccagata ttggctgcn tttgttnangg tcaaattact cacaaacttt 540  
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<210> 24

<211> 160

<212> PRT

<213> Triticum aestivum

<400> 24

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20 25 30

Thr Ile Arg Pro Phe Ser Lys Arg Leu Tyr Arg Gln Ile Asn Val Phe  
35 40 45

Leu Ala Glu Leu Leu Trp Leu Gln Leu Ile Trp Leu Val Asp Trp Trp  
50 55 60

Ala Gly Ile Lys Val Gln Val Tyr Ala Asp Pro Glu Thr Trp Lys Leu  
65 70 75 80

Met Gly Lys Glu His Ala Leu Leu Ile Ser Asn His Arg Ser Asp Ile  
85 90 95

Asp Trp Leu Val Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly  
100 105 110

Ser Ala Ile Ala Ile Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile  
115 120 125

Gly Trp Ser Met Trp Phe Ala Glu Tyr Ser Phe Gly Glu Asn Trp Gln  
130 135 140

Arg Met Lys Asn Thr Lys Ser Gly Leu Lys Val Lys Thr Pro Asp Ile  
145 150 155 160

<210> 25

<211> 1337

<212> DNA

<213> Catalpa speciosa

<400> 25

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tccgcctgctg tcgatggctc gatatttcac caactctaac tgaggcagct ggtgccattg 180

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taaggtaat	agtgttgaca	ataggatgga	ttatatttct	ctcatgctat	ttccctgtgc	360
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ccagcatgcg	gcctaagcag	gttttgg	ctaatacac	atccatgatt	gatttcattt	540
tttggaaaca	aatgactgca	tttgcagtga	ttatgcagaa	gcattcctggg	tggtaggac	600
tattgcagag	cactatTTT	gagagtctag	gatgtatctg	gttcaaccgg	tcagagtcca	660
aggaccgtga	aattgttgc	aaaaagctaa	gagatcatgt	ccatggcgct	gataataatc	720
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agcAAAGCA	acAAAGCTC	gcagagtca	ttctccatca	cctggaaAGAG	aaatagattt	1140
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aaaaaaaaaa	aaaaaaaaaa					1337

<210> 26

<211> 371

<212> PRT

<213> Catalpa speciosa

<400> 26

Met	Ser	Lys	Leu	Lys	Thr	Ser	Ser	Ser	Glu	Leu	Asp	Leu	Asp	His	Pro
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Asn	Ile	Glu	Asp	Tyr	Leu	Pro	Ser	Gly	Ser	Ile	Gln	Glu	Pro	His	Gly
						20			25			30			

Lys	Leu	Arg	Leu	Arg	Asp	Leu	Leu	Asp	Ile	Ser	Pro	Thr	Leu	Thr	Glu
							35		40			45			

Ala	Ala	Gly	Ala	Ile	Val	Asp	Asp	Ser	Phe	Thr	Arg	Cys	Phe	Lys	Ser
						50		55			60				

Asn	Pro	Pro	Glu	Pro	Trp	Asn	Trp	Asn	Ile	Tyr	Leu	Phe	Pro	Leu	Trp
						65		70			75			80	

Cys	Leu	Gly	Val	Val	Val	Arg	Tyr	Gly	Leu	Leu	Phe	Pro	Leu	Arg	Val
						85			90			95			

Ile	Val	Leu	Thr	Ile	Gly	Trp	Ile	Ile	Phe	Leu	Ser	Cys	Tyr	Phe	Pro
						100		105			110				

Val	His	Phe	Leu	Leu	Lys	Gly	His	Asp	Lys	Leu	Arg	Lys	Lys	Leu	Glu
						115		120			125				

Arg	Gly	Leu	Val	Glu	Leu	Met	Cys	Ser	Phe	Phe	Val	Ala	Ser	Trp	Thr
						130		135			140				

Gly	Val	Val	Lys	Tyr	His	Gly	Pro	Arg	Pro	Ser	Met	Arg	Pro	Lys	Gln
						145		150			155			160	

Val	Phe	Val	Ala	Asn	His	Thr	Ser	Met	Ile	Asp	Phe	Ile	Val	Leu	Glu
						165		170			175				

Gln Met Thr Ala Phe Ala Val Ile Met Gln Lys His Pro Gly Trp Val  
180 185 190

Gly Leu Leu Gln Ser Thr Ile Leu Glu Ser Leu Gly Cys Ile Trp Phe  
195 200 205

Asn Arg Ser Glu Ser Lys Asp Arg Glu Ile Val Ala Lys Lys Leu Arg  
210 215 220

Asp His Val His Gly Ala Asp Asn Asn Pro Leu Leu Ile Phe Pro Glu  
225 230 235 240

Gly Thr Cys Val Asn Asn His Tyr Thr Val Met Phe Lys Lys Gly Ala  
245 250 255

Phe Glu Leu Gly Cys Thr Val Cys Pro Ile Ala Ile Lys Tyr Asn Lys  
260 265 270

Ile Phe Val Asp Ala Phe Trp Asn Ser Arg Lys Gln Ser Phe Thr Met  
275 280 285

His Leu Leu Gln Leu Met Thr Ser Trp Ala Val Val Cys Asp Val Trp  
290 295 300

Tyr Leu Glu Pro Gln Asn Leu Lys Pro Gly Glu Thr Pro Ile Glu Phe  
305 310 315 320

Ala Glu Arg Val Arg Gly Ile Ile Ser Val Arg Ala Gly Leu Lys Lys  
325 330 335

Val Pro Trp Asp Gly Tyr Leu Lys Tyr Ser Arg Pro Ser Pro Lys His  
340 345 350

Arg Glu Arg Lys Gln Gln Ser Phe Ala Glu Ser Val Leu His His Leu  
355 360 365

Glu Glu Lys  
370

<210> 27  
<211> 1582  
<212> DNA  
<213> Zea mays

<400> 27  
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ggaccggcca aacctggagg actacctccc gcccgaactcg ctcccgccagg aggcgcggcccg 180  
gaatctccat ctgcgcgatc tgctggacat ctcgcggatg ctcaccgagg cagcgggtgc 240  
cattgtcgat gactccttca cacggtgctt taagtcaaat tctccagagc catggaaattg 300  
gaacatatat ctgttccct tatggtgctt tggtagta ataagatatg gattactctt 360  
cccactgagg tccttaacgc ttgcaatagg atggtagca tttttgctg cttttttcc 420  
tgtccatttc ctattgaaag gtcaagacaa gttgagaagt aaaattgaga ggaagtgg 480  
tgaaatgtg tgcagtgttt ttgttgcttc atggactgga gttatcaagt atcatggacc 540  
acgcccggc acacgaccc acatggatatt cggtgcaaac catacatcgat tgatagattt 600  
cattattctg gagcaaatga cagcattgc tgtcatcatg cagaagcattc ctggatgggt 660  
tggatttatt cagaagacta tcttggaaag tgtcgggtgc atctggtttta atcgtaatga 720  
tctccgggac cgtgaagttt cggcacggaa gttacgtgat catgttcaac aaccagacaa 780  
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caagaagggt gcctttgagc ttggctgcgc tgtatgtcca atagctatca agtacaataa 900

aatatttgtt gatgcctttt ggaacagtaa gaagcaatct tttacaatgc acttggtccg 960  
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 aaaaaaaaaaaa aaaaaaaaaaaa ag 1582

<210> 28  
 <211> 371  
 <212> PRT  
 <213> Zea mays

<400> 28  
 Met Ala Thr Ser Ser Val Ala Ala Asp Met Glu Leu Asp Arg Pro Asn  
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Leu Glu Asp Tyr Leu Pro Pro Asp Ser Leu Pro Gln Glu Ala Pro Arg  
 20 25 30

Asn Leu His Leu Arg Asp Leu Leu Asp Ile Ser Pro Val Leu Thr Glu  
 35 40 45

Ala Ala Gly Ala Ile Val Asp Asp Ser Phe Thr Arg Cys Phe Lys Ser  
 50 55 60

Asn Ser Pro Glu Pro Trp Asn Trp Asn Ile Tyr Leu Phe Pro Leu Trp  
 65 70 75 80

Cys Phe Gly Val Val Ile Arg Tyr Gly Leu Leu Phe Pro Leu Arg Ser  
 85 90 95

Leu Thr Leu Ala Ile Gly Trp Leu Ala Phe Phe Ala Ala Phe Phe Pro  
 100 105 110

Val His Phe Leu Leu Lys Gly Gln Asp Lys Leu Arg Ser Lys Ile Glu  
 115 120 125

Arg Lys Leu Val Glu Met Met Cys Ser Val Phe Val Ala Ser Trp Thr  
 130 135 140

Gly Val Ile Lys Tyr His Gly Pro Arg Pro Ser Thr Arg Pro His Gln  
 145 150 155 160

Val Phe Val Ala Asn His Thr Ser Met Ile Asp Phe Ile Ile Leu Glu  
 165 170 175

Gln Met Thr Ala Phe Ala Val Ile Met Gln Lys His Pro Gly Trp Val  
 180 185 190

Gly Phe Ile Gln Lys Thr Ile Leu Glu Ser Val Gly Cys Ile Trp Phe  
 195 200 205

Asn Arg Asn Asp Leu Arg Asp Arg Glu Val Thr Ala Arg Lys Leu Arg  
 210 215 220

Asp His Val Gln Gln Pro Asp Asn Asn Pro Leu Leu Ile Phe Pro Glu  
225 230 235 240

Gly Thr Cys Val Asn Asn Gln Tyr Thr Val Met Phe Lys Lys Gly Ala  
245 250 255

Phe Glu Leu Gly Cys Ala Val Cys Pro Ile Ala Ile Lys Tyr Asn Lys  
260 265 270

Ile Phe Val Asp Ala Phe Trp Asn Ser Lys Lys Gln Ser Phe Thr Met  
275 280 285

His Leu Val Arg Leu Met Thr Ser Trp Ala Val Val Cys Asp Val Trp  
290 295 300

Tyr Leu Pro Pro Gln Tyr Leu Arg Glu Gly Glu Thr Ala Ile Ala Phe  
305 310 315 320

Ala Glu Arg Val Arg Asp Met Ile Ala Ala Arg Ala Gly Leu Lys Lys  
325 330 335

Val Pro Trp Asp Gly Tyr Leu Lys His Asn Arg Pro Ser Pro Lys His  
340 345 350

Thr Glu Glu Lys Gln Arg Ile Phe Ala Glu Ser Val Leu Met Arg Leu  
355 360 365

Glu Glu Lys  
370

<210> 29

<211> 1422

<212> DNA

<213> Oryza sativa

<400> 29

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gctttaagtc aaattctcca gagccatggaa attggaacat ttatatttcc ccattgtgg 300  
gcttgggagt agtgataaga tacggaatac tattcccgct gaggggccta actcttctag 360  
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cttgtgttaa caaccagtac actgtcatgt tcaagaaggg tgcttttagt cttggctgtg 840  
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1422

<210> 30

<211> 370

<212> PRT

<213> Oryza sativa

<400> 30

Met Ala Thr Ser Ser Val Ala Gly Asp Ile Glu Leu Asp Arg Pro Asn  
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Leu Glu Asp Tyr Leu Pro Ser Asp Ser Leu Pro Gln Glu Phe Pro Arg  
20 25 30

Asn Leu His Leu Arg Asp Leu Leu Asp Ile Ser Pro Val Leu Thr Glu  
35 40 45

Ala Ala Gly Ala Ile Val Asp Asp Ser Phe Thr Arg Cys Phe Lys Ser  
50 55 60

Asn Ser Pro Glu Pro Trp Asn Trp Asn Ile Tyr Leu Phe Pro Leu Trp  
65 70 75 80

Cys Leu Gly Val Val Ile Arg Tyr Gly Ile Leu Phe Pro Leu Arg Gly  
85 90 95

Leu Thr Leu Leu Val Gly Trp Leu Ala Phe Phe Ala Ala Phe Phe Pro  
100 105 110

Val His Phe Leu Leu Lys Gly Gln Lys Met Arg Ser Lys Ile Glu Arg  
115 120 125

Lys Leu Val Glu Met Met Cys Ser Val Phe Val Ala Ser Trp Thr Gly  
130 135 140

Val Ile Lys Tyr His Gly Pro Arg Pro Ser Thr Arg Pro His Gln Val  
145 150 155 160

Phe Val Ala Asn His Thr Ser Met Ile Asp Phe Ile Ile Leu Glu Gln  
165 170 175

Met Thr Ala Phe Ala Val Ile Met Gln Lys His Pro Gly Trp Val Gly  
180 185 190

Phe Ile Gln Lys Thr Ile Leu Glu Ser Val Gly Cys Ile Trp Phe Asn  
195 200 205

Arg Asn Asp Leu Lys Asp Arg Glu Val Val Ala Lys Lys Leu Arg Asp  
210 215 220

His Val Gln His Pro Asp Ser Asn Pro Leu Leu Ile Phe Pro Glu Gly  
225 230 235 240

Thr Cys Val Asn Asn Gln Tyr Thr Val Met Phe Lys Lys Gly Ala Phe  
245 250 255

Glu Leu Gly Cys Ala Val Cys Pro Ile Ala Ile Lys Tyr Asn Lys Ile  
260 265 270

Phe Val Asp Ala Phe Trp Asn Ser Lys Lys Gln Ser Phe Thr Met His  
275 280 285

Leu Val Arg Leu Met Thr Ser Trp Ala Val Val Cys Asp Val Trp Tyr  
290 295 300

Leu Glu Pro Gln Tyr Leu Arg Asp Gly Glu Thr Ala Ile Glu Phe Ala  
305 310 315 320

Glu Arg Val Arg Asp Met Ile Ala Ala Arg Ala Gly Leu Lys Lys Val  
325 330 335

Pro Trp Asp Gly Tyr Leu Lys His Asn Arg Pro Ser Pro Lys His Thr  
340 345 350

Glu Glu Lys Gln Arg Ile Phe Ala Asp Ser Val Leu Arg Arg Leu Glu  
355 360 365

Glu Ser  
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<210> 31

<211> 1392

<212> DNA

<213> Sorghum

<400> 31

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acggcatgt tcaagaaggg tgccttgag cttgggtgtg ctgtctgtcc aatagctatc 720  
aaatacaata aaatattttgt tgatgcctt tggAACAGTA agaagcaatc ttttacatgt 780  
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aaaaaaaaaa aa 1392

<210> 32

<211> 343

<212> PRT

<213> Sorghum

<400> 32

Ala Arg Ala Arg Asn Leu His Leu Arg Asp Leu Leu Asp Ile Ser Pro  
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Val	Leu	Thr	Glu	Ala	Ala	Gly	Ala	Ile	Val	Asp	Asp	Ser	Phe	Thr	Arg
				20					25				30		
Cys	Phe	Lys	Ser	Asn	Ser	Pro	Glu	Pro	Trp	Asn	Trp	Asn	Ile	Tyr	Leu
				35			40					45			
Phe	Pro	Leu	Trp	Cys	Phe	Gly	Val	Val	Ile	Arg	Tyr	Gly	Leu	Leu	Phe
				50			55			60					
Pro	Leu	Arg	Ser	Leu	Thr	Leu	Ala	Ile	Gly	Trp	Leu	Ala	Phe	Phe	Ala
				65			70			75			80		
Ala	Phe	Phe	Pro	Val	His	Phe	Leu	Leu	Lys	Gly	Gln	Asp	Lys	Leu	Arg
				85				90				95			
Asn	Lys	Ile	Glu	Arg	Lys	Leu	Val	Glu	Met	Met	Cys	Ser	Val	Phe	Val
				100				105				110			
Ala	Ser	Trp	Thr	Gly	Val	Ile	Lys	Tyr	His	Gly	Pro	Arg	Pro	Ser	Thr
				115			120			125					
Arg	Pro	His	Gln	Val	Phe	Val	Ala	Asn	His	Thr	Ser	Met	Ile	Asp	Phe
				130			135			140					
Ile	Ile	Leu	Glu	Gln	Met	Thr	Ala	Phe	Ala	Val	Ile	Met	Gln	Lys	His
				145			150			155			160		
Pro	Gly	Trp	Val	Gly	Phe	Ile	Gln	Lys	Thr	Ile	Leu	Glu	Ser	Val	Gly
				165				170				175			
Cys	Ile	Trp	Phe	Asn	Arg	Asn	Asp	Leu	Arg	Asp	Arg	Glu	Val	Thr	Ala
				180				185			190				
Arg	Lys	Leu	Arg	Asp	His	Val	Gln	His	Pro	Asp	Lys	Asn	Pro	Leu	Leu
				195			200			205					
Ile	Phe	Pro	Glu	Gly	Thr	Cys	Val	Asn	Asn	Gln	Tyr	Thr	Val	Met	Phe
				210			215			220					
Lys	Lys	Gly	Ala	Phe	Glu	Leu	Gly	Cys	Ala	Val	Cys	Pro	Ile	Ala	Ile
				225			230			235			240		
Lys	Tyr	Asn	Lys	Ile	Phe	Val	Asp	Ala	Phe	Trp	Asn	Ser	Lys	Gln	
				245				250				255			
Ser	Phe	Thr	Met	His	Leu	Val	Arg	Leu	Met	Thr	Ser	Trp	Ala	Val	Val
				260			265			270					
Cys	Asp	Val	Trp	Tyr	Leu	Glu	Pro	Gln	Tyr	Leu	Arg	Glu	Gly	Glu	Thr
				275			280			285					
Ala	Ile	Ala	Phe	Ala	Glu	Arg	Val	Arg	Asp	Met	Ile	Ala	Ala	Arg	Ala
				290			295			300					
Gly	Leu	Lys	Lys	Val	Pro	Trp	Asp	Gly	Tyr	Leu	Lys	His	Asn	Arg	Pro
				305			310			315			320		
Ser	Pro	Lys	His	Thr	Glu	Glu	Lys	Gln	Arg	Ile	Phe	Ala	Glu	Ser	Val
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Leu Arg Arg Leu Glu Glu Lys  
340

<210> 33  
<211> 1466  
<212> DNA  
<213> Glycine max

<400> 33  
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tctattgcca cgttggatc gaaaagtcta gtttaaccac acgtttgtgg ttgttagtgaa 180  
agcgtaacga agatgaatgg cattggaaaa ctcaaatacg cgagttctga attggacctt 240  
cacattgaag attacctacc ttctggatcc agtgttcaac aagaacggca tggcaagctc 300  
cgactgtgtg atttgctaga catttctcct agtctatctg aggccagcacg tgccattgt 360  
gatgatacat tcacaagggtg ctcaagtca aatcctccag aaccttgaa ctggaatgtt 420  
tatttggttc ctttgggtg ctgtggagtt gtgggtcgat atttgatttt gttccctatt 480  
aggattctag tgggtgcatt agatggatt atatttctt cagccttcat tccagtgac 540  
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agtatccgac caaaacaggt ttttggcc aatcataactt ccatgattga tttcattatc 720  
ttagaacaga tgactgcatt tgctgttatt atgcagaagc atcctggatg ggtggattt 780  
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ggaaagcaac aaatattcgc tgagtctgtg ttgcggcgct ttgagggaaa ataatgtata 1320  
tcttttact tttcagtaa tgatttctc caaccctgt ttgtactcca cttactacta 1380  
tgatatacat gtatctta catgaaattt cctgaaaattt ttccatgacc aaaaaaaaaa 1440  
aaaaaaaaact cgagactagt tctctc 1466

<210> 34  
<211> 373  
<212> PRT  
<213> Glycine max

<400> 34  
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His Ile Glu Asp Tyr Leu Pro Ser Gly Ser Ser Val Gln Gln Glu Arg  
20 25 30  
  
His Gly Lys Leu Arg Leu Cys Asp Leu Leu Asp Ile Ser Pro Ser Leu  
35 40 45  
  
Ser Glu Ala Ala Arg Ala Ile Val Asp Asp Thr Phe Thr Arg Cys Phe  
50 55 60  
  
Lys Ser Asn Pro Pro Glu Pro Trp Asn Trp Asn Val Tyr Leu Phe Pro  
65 70 75 80  
  
Leu Trp Cys Cys Gly Val Val Val Arg Tyr Leu Ile Leu Phe Pro Ile  
85 90 95

Arg Ile Leu Val Leu Ala Leu Gly Trp Ile Ile Phe Leu Ser Ala Phe  
 100 105 110  
 Ile Pro Val His Ser Leu Leu Lys Gly Asn Asp Asp Leu Arg Lys Lys  
 115 120 125  
 Ile Glu Arg Cys Leu Val Glu Met Met Cys Ser Phe Phe Val Ala Ser  
 130 135 140  
 Trp Thr Gly Val Val Lys Tyr His Gly Pro Arg Pro Ser Ile Arg Pro  
 145 150 155 160  
 Lys Gln Val Phe Val Ala Asn His Thr Ser Met Ile Asp Phe Ile Ile  
 165 170 175  
 Leu Glu Gln Met Thr Ala Phe Ala Val Ile Met Gln Lys His Pro Gly  
 180 185 190  
 Trp Val Gly Leu Leu Gln Ser Thr Ile Leu Glu Ser Val Gly Cys Ile  
 195 200 205  
 Trp Phe Asn Arg Thr Glu Ala Lys Asp Arg Glu Ile Val Ala Arg Lys  
 210 215 220  
 Leu Arg Asp His Val Leu Gly Ala Asn Asn Asn Pro Leu Leu Ile Phe  
 225 230 235 240  
 Pro Glu Gly Thr Cys Val Asn Asn His Tyr Ser Val Met Phe Lys Lys  
 245 250 255  
 Gly Ala Phe Glu Leu Gly Cys Thr Ile Cys Pro Val Ala Ile Lys Tyr  
 260 265 270  
 Asn Lys Ile Phe Val Asp Ala Phe Trp Asn Ser Arg Lys Gln Ser Phe  
 275 280 285  
 Thr Thr His Leu Leu Gln Leu Met Thr Ser Trp Ala Val Val Cys Asp  
 290 295 300  
 Val Trp Tyr Leu Glu Pro Gln Asn Leu Lys Pro Gly Glu Thr Pro Ile  
 305 310 315 320  
 Glu Phe Ala Glu Arg Val Arg Asp Ile Ile Ser His Arg Ala Gly Leu  
 325 330 335  
 Lys Lys Val Pro Trp Asp Gly Tyr Leu Lys Tyr Ser Arg Pro Ser Pro  
 340 345 350  
 Lys His Arg Glu Gly Lys Gln Gln Ile Phe Ala Glu Ser Val Leu Arg  
 355 360 365  
 Arg Phe Glu Glu Lys  
 370

<210> 35  
 <211> 1384  
 <212> DNA  
 <213> Catalpa speciosa

<400> 35

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cggctctgaag	aggtggaaagg	acctggggct	attgtatcca	atcatatatc	ttatataagat	180
atccctgtatc	acatgtcttc	ctctttccca	agtttcgttt	ccaagagatc	cgtcgctaaa	240
cttccccttg	ttggtcttgt	gagcaagtgt	cttggttgtg	tatatgtaca	gcgtgagtt	300
aagtctcg	atttcaaggg	ggtatcaggt	gttgcactg	aaagaattca	agaagctcat	360
caaaataagt	ttgctccaaa	gatgataatt	ttcccagaag	gcacaactac	aatggggac	420
ttcctccttc	cattcaagac	tggtgcattt	ttggcaaagg	ctccagact	tcctgtcatt	480
ttaagatatt	cgtaccagag	atttagtccc	gcgtggact	ctatttctgg	ggctcgccat	540
gtgattcttc	ttctctgtca	gttgtaaat	tacattgaag	tgacacattt	gcctgtttat	600
catccgtccg	aacaagaaaa	ggaagatccc	aagctttcg	ctgaaaatgt	taggcttctg	660
atggctcg	aggtaattt	gattttcg	gatattggat	tggcggagaa	acgagtttat	720
catgctgctc	tcaatggttt	actttgtcaa	agataatcca	gcttcgctat	attgattgt	780
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ggtcattgt	cttcatcg	tatacgattt	ctaactatta	tctggacatc	ttagttactg	900
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gagttcg	ttttagg	ataaaatcgca	tttctcta	agtttgttct	actgggtacg	1140
gtattagtt	cccttgtat	atagcacaat	gcaaatgctg	tagttaacta	ctttgtttt	1200
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ttggattagc	atagttaa	gtgaaatatg	tagtggtgcc	tgagaatggt	cttggattgg	1320
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<210> 36

<211> 251

<212> PRT

<213> Catalpa speciosa

<400> 36

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Tyr	Trp	Ile	Gly	Glu	Thr	Ser	Lys	Gly	Ile	Glu	Val	Asp	Gly	Gln	Gly
					20				25				30		

Asn	Asn	Glu	Ser	Ala	Ser	Arg	Asn	Arg	Ser	Glu	Glu	Val	Glu	Gly	Pro
						35		40				45			

Gly	Ala	Ile	Val	Ser	Asn	His	Ile	Ser	Tyr	Ile	Asp	Ile	Leu	Tyr	His
						50		55			60				

Met	Ser	Ser	Ser	Phe	Pro	Ser	Phe	Val	Ser	Lys	Arg	Ser	Val	Ala	Lys
						65		70		75			80		

Leu	Pro	Leu	Val	Gly	Leu	Val	Ser	Lys	Cys	Leu	Gly	Cys	Val	Tyr	Val
						85			90			95			

Gln	Arg	Glu	Leu	Lys	Ser	Ser	Asp	Phe	Lys	Gly	Val	Ser	Gly	Val	Val
						100		105			110				

Thr	Glu	Arg	Ile	Gln	Glu	Ala	His	Gln	Asn	Lys	Phe	Ala	Pro	Lys	Met
						115		120			125				

Ile	Ile	Phe	Pro	Glu	Gly	Thr	Thr	Asn	Gly	Asp	Phe	Leu	Leu	Pro	
						130		135			140				

Phe Lys Thr Gly Ala Phe Leu Ala Lys Ala Pro Val Leu Pro Val Ile  
145 150 155 160

Leu Arg Tyr Ser Tyr Gln Arg Phe Ser Pro Ala Trp Asp Ser Ile Ser  
165 170 175

Gly Ala Arg His Val Ile Leu Leu Cys Gln Phe Val Asn Tyr Ile  
180 185 190

Glu Val Thr His Leu Pro Val Tyr His Pro Ser Glu Gln Glu Lys Glu  
195 200 205

Asp Pro Lys Leu Phe Ala Glu Asn Val Arg Leu Leu Met Ala Arg Glu  
210 215 220

Gly Asn Leu Ile Leu Ser Asp Ile Gly Leu Ala Glu Lys Arg Val Tyr  
225 230 235 240

His Ala Ala Leu Asn Gly Leu Leu Cys Gln Arg  
245 250

<210> 37

<211> 1042

<212> DNA

<213> Triticum aestivum

<400> 37

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cgaggatgta cctaaagatc actatgaaga actggaaaga ccaggggcga ttgtatctaa 180  
tcatgtgtca tatgtggaca ttctttatca tatgtcagct tcttctccga gttttgttgc 240  
taagaactca gtgtccaagt tgccgttgc tggtctcata agcaaatgtc ttgggtgtcat 300  
ttttgttcaa cgagaatcca aatgttcaga ttctaaaggt gtctcaggtg ctgtaactga 360  
aaggctccat gaggttccac aagacgagaa ttcccctatg atcttactct tccctgaggg 420  
tactactacg aatggggatt accttctccc attaaagaca ggacgccttc ttgcaagggc 480  
accattgcaa cctgtatatt ttagatatcc ttacaggaga tttagtccag cctgggactc 540  
catggatggg gcacgtcatg tgggggtgc cctctgtcaa tttgcaaatt acatagaggt 600  
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caacaacgtc agaaaattgc ttgcgactga gggtaattta gttctgtcta atcttgggct 720  
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gaaagatgat tgaaagccct tgcataact tctgtacact atctgttgag gtgattgtaa 840  
gaatgtatgc caactttagc tgatcatgtg attcatggtt tctctgtttg aggagtatgt 900  
tgattgatga aaacattata cctatttga gatgaattcc ctccttatac tacattgtat 960  
agaaaaccatt aaacattata gtcataataat aatgtctggc ataattgttt tgcttggca 1020  
aaaaaaaaaaaa aaaaaaaaaaa aa 1042

<210> 38

<211> 261

<212> PRT

<213> Triticum aestivum

<400> 38

Gln Gly Leu Arg Arg Glu Ala Val Leu Arg Ala Gly Arg Val Leu Ser  
1 5 10 15

Arg Ala Met Leu Phe Val Phe Gly Phe Tyr Trp Ile Pro Val Ser Asp  
20 25 30

Arg Ser Phe Pro Asn Ala Glu Asp Val Pro Lys Asp His Tyr Glu Glu  
35 40 45

Leu Glu Arg Pro Gly Ala Ile Val Ser Asn His Val Ser Tyr Val Asp  
       50                         55                         60

Ile Leu Tyr His Met Ser Ala Ser Ser Pro Ser Phe Val Ala Lys Asn  
       65                         70                         75                         80

Ser Val Ser Lys Leu Pro Leu Ile Gly Leu Ile Ser Lys Cys Leu Gly  
       85                         90                         95

Cys Ile Phe Val Gln Arg Glu Ser Lys Cys Ser Asp Ser Lys Gly Val  
       100                        105                         110

Ser Gly Ala Val Thr Glu Arg Leu His Glu Val Ser Gln Asp Glu Asn  
       115                        120                         125

Ser Pro Met Ile Leu Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly Asp  
       130                        135                         140

Tyr Leu Leu Pro Phe Lys Thr Gly Ala Phe Leu Ala Arg Ala Pro Leu  
       145                        150                         155                         160

Gln Pro Val Ile Leu Arg Tyr Pro Tyr Arg Arg Phe Ser Pro Ala Trp  
       165                        170                         175

Asp Ser Met Asp Gly Ala Arg His Val Phe Leu Leu Leu Cys Gln Phe  
       180                        185                         190

Ala Asn Tyr Ile Glu Val Val Arg Leu Pro Val Tyr Tyr Pro Ser Glu  
       195                        200                         205

Gln Glu Lys Gln Asp Pro Arg Val Tyr Ala Asn Asn Val Arg Lys Leu  
       210                        215                         220

Leu Ala Thr Glu Gly Asn Leu Val Leu Ser Asn Leu Gly Leu Ala Glu  
       225                        230                         235                         240

Lys Arg Val Tyr His Ala Ala Leu Asn Gly Asn Ser Pro Arg Ala Leu  
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His Gln Lys Asp Asp  
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<210> 39  
 <211> 1459  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (203)  
 <223> n = a, c, g, or t

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 caggttatat atgttgacag attctcacca gcttctcgga aggctgctgt aaatgaaata   180  
 aagagaaaagg cagcttgcaa tancttcccg cgggtcctgt tattccctga aggcaccaca   240  
 acaaatggga gatctctgat ttcggtccaa catggtgctgt tcataacctgg ctaccctgtt   300  
 caacctgtt ttgtccatata tccacatgtg cactttgatc aatcatgggg aaatatatcg   360

ttattaaagc tcatgttcaa gatgttcaca cagttcata atttcata ggttagagtac 420  
 cttcctgttg tctaccctcc tgagatcaag caagagaatg cccttcattt tgcagaggat 480  
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 tatgattatg gcacgagcag tagaagctgg aaaggtaac tgctcaaatt atatggaga 600  
 aatggcttgg gttaaagatg tttacggat aagcacagca gaagtatgg aactattgga 660  
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 accactgttc cagggttcct gcgagaccgc ctttgagaag tgccgggtc ctgaaacgtc 900  
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 aaaaaaaaaa aaaaaaaaaa 1459

<210> 40  
 <211> 204  
 <212> PRT  
 <213> Zea mays

<220>  
 <221> UNSURE  
 <222> (68)  
 <223> Xaa = any amino acid

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 Leu Phe Pro Thr Ile Val Ser Ser Glu Ser His Asp Ala Leu Pro Phe  
       20                         25                                 30  
  
 Val Gly Thr Ile Ile Arg Ala Met Gln Val Ile Tyr Val Asp Arg Phe  
       35                         40                                 45  
  
 Ser Pro Ala Ser Arg Lys Ala Ala Val Asn Glu Ile Lys Arg Lys Ala  
       50                         55                                 60  
  
 Ala Cys Asn Xaa Phe Pro Arg Val Leu Leu Phe Pro Glu Gly Thr Thr  
       65                         70                                 75                         80  
  
 Thr Asn Gly Arg Phe Leu Ile Ser Phe Gln His Gly Ala Phe Ile Pro  
       85                         90                                 95  
  
 Gly Tyr Pro Val Gln Pro Val Val His Tyr Pro His Val His Phe  
       100                         105                                 110  
  
 Asp Gln Ser Trp Gly Asn Ile Ser Leu Leu Lys Leu Met Phe Lys Met  
       115                         120                                 125  
  
 Phe Thr Gln Phe His Asn Phe Met Glu Val Glu Tyr Leu Pro Val Val  
       130                         135                                 140  
  
 Tyr Pro Pro Glu Ile Lys Gln Glu Asn Ala Leu His Phe Ala Glu Asp  
       145                         150                                 155                         160

Thr Ser Tyr Ala Met Ala Arg Ala Leu Asn Ala Leu Pro Thr Tyr Tyr  
165 170 175

Ser Trp Arg Phe Tyr Asp Tyr Gly Thr Ser Ser Arg Ser Trp Lys Gly  
180 185 190

Glu Leu Leu Lys Leu Tyr Gly Arg Asn Gly Leu Gly  
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<210> 41

<211> 2115

<212> DNA

<213> Oryza sativa

<400> 41

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accaacggcc acgcggggca ccataaccac gacgacgacg acgaggagtc gccaacggtg 180  
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aaaaaaaaaaa aaaaa 2115

<210> 42

<211> 255

<212> PRT

<213> Oryza sativa

<400> 42  
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 Ser Asp Ser Ile Ser Pro Thr Pro Thr Thr Asn Gly His Ala Gly His  
   20              25                           30  
  
 His Asn His Asp Asp Asp Glu Glu Ser Pro Thr Val Cys Gly Gly  
   35              40                           45  
  
 Asp Gly Gly Gly Gly Asp Pro Phe Ala Phe Leu Ser Glu Asp Arg  
   50              55                           60  
  
 Pro Ala Trp Trp Ser Pro Arg Gly Val Ser Pro Ala Asp Pro Phe Arg  
   65              70                           75                           80  
  
 Asn Gly Thr Pro Gly Trp Cys Gly Ala Tyr Glu Leu Val Arg Ala Leu  
   85              90                           95  
  
 Val Cys Ala Pro Val Ala Ala Ala Arg Leu Val Leu Phe Gly Leu Ser  
   100             105                           110  
  
 Ile Ala Val Gly Tyr Ala Ala Thr Trp Val Ala Leu Arg Gly Trp Val  
   115             120                           125  
  
 Asp Val Arg Glu Arg Ala Ala Gln Glu Gly Ala Gly Pro Met Pro Ala  
   130             135                           140  
  
 Trp Arg Arg Arg Leu Met Trp Ile Thr Arg Ile Ser Ala Arg Cys Ile  
   145             150                           155                           160  
  
 Leu Phe Ser Phe Gly Tyr His Trp Ile Arg Arg Lys Gly Lys Pro Ala  
   165             170                           175  
  
 Pro Arg Glu Leu Ala Pro Ile Val Val Ser Asn His Val Ser Tyr Ile  
   180             185                           190  
  
 Glu Pro Ile Tyr Phe Phe Tyr Glu Leu Phe Pro Thr Ile Val Ser Ser  
   195             200                           205  
  
 Asp Ser His Asp Ser Ile Pro Phe Val Gly Thr Ile Ile Arg Ala Met  
   210             215                           220  
  
 Gln Val Ile Tyr Val Asp Arg Phe Ser Pro Ala Ser Arg Lys Ser Ala  
   225             230                           235                           240  
  
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 <213> Glycine max  
  
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 ctggcggcgc tgccgctcgc gctgttcggg ctctgcctcg cggtgggta cgtggcgacg   180  
 aaggtggcgc tggcagggtg gaaggacaag gagaatcca tgcccaagtg gaggtgttagg   240  
 gttatgtgga tcacgcgtt gtgcgccaga tgtattctct tctccttgg ctatcagtgg   300

ataaaacgga aaggaaaacc tgcaccaagg gaaattgctc caataattgt atctaaccat 360  
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cctgggtaa tgtttcttg gaaaaagctt tggcataat gttcactcaa tttcacaact 780  
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ctgtggactt tctggataaa ttcttggcca tgaatcctga tcccagtggt cgtgttcaat 1080  
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cattcattga tgggagaag agtgggacaa ttacggttcag acagttcttgc tatggatctg 1200  
cccatgttat gtcaccaacct gggttcgatc aaaccttga agaagcctt gctggctgtg 1260  
gcgggtcagt aaagacctat gttgttgaac aagagttacg agatttcatc caacctgcta 1320  
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tgtgatggat ggatttcaca ttccaggctt ttgtggacta caaagaaaag aaatgggtag 1560  
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tggtcaggg accatgctga catttaggtt ccatgtgggtt catgtaaagt ttgaaccaac 1860  
gtgtcaattt gtaacaaaca ttataactgt atttttttc aaagatgtga acatgaagaa 1920  
agtaatgtaa ttatggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaactcgag 1980  
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g 2041

<210> 44  
<211> 228  
<212> PRT  
<213> Glycine max

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20									25					30		
Ala	Lys	Thr	Ala	Leu	Cys	Leu	Pro	Leu	Ala	Ala	Leu	Arg	Leu	Ala	Leu	
35									40					45		
Phe	Gly	Leu	Cys	Leu	Ala	Val	Gly	Tyr	Val	Ala	Thr	Lys	Val	Ala	Leu	
50									55					60		
Ala	Gly	Trp	Lys	Asp	Lys	Glu	Asn	Pro	Met	Pro	Lys	Trp	Arg	Cys	Arg	
65									70					75		80
Val	Met	Trp	Ile	Thr	Arg	Leu	Cys	Ala	Arg	Cys	Ile	Leu	Phe	Ser	Phe	
											85			90		95
Gly	Tyr	Gln	Trp	Ile	Lys	Arg	Lys	Gly	Lys	Pro	Ala	Pro	Arg	Glu	Ile	
									100					105		110
Ala	Pro	Ile	Ile	Val	Ser	Asn	His	Val	Ser	Tyr	Ile	Glu	Pro	Ile	Phe	
									115					120		125

Tyr Phe Tyr Glu Leu Phe Pro Thr Ile Val Ala Ala Glu Ser His Asp  
130 135 140

Ser Ile Pro Phe Val Gly Thr Ile Ile Arg Ala Met Gln Val Ile Tyr  
145 150 155 160

Val Asn Arg Phe Leu Pro Ser Ser Arg Lys Gln Ala Val Arg Glu Ile  
165 170 175

Lys Lys Ser Ala Phe Lys Glu Leu Asn Asn Arg Glu Gly Pro Leu Val  
180 185 190

Ile Asn Phe Leu Glu Tyr Tyr Phe Pro Arg Glu Gln Gln Leu Met  
195 200 205

Ala Gly Thr Leu Ser Pro Ser Asn Leu Val His Leu Ser Leu Asp Thr  
210 215 220

Gln Ser Ser Leu  
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<210> 45

<211> 1502

<212> DNA

<213> Zea mays

<400> 45

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gagcgtggc ggcagtgaga ttagcagcga agacatggcc gccgccagtc cgctcctctc 180  
gtcgtcctcc ccctccccctt cccctccgc agcccccgtg ctggagagca tagaggaact 240  
ggaccggaag tacgcaccgt acgcgcggcg ggacgcgtac ggaccgatgg ggctcgccc 300  
cgtgagcgcgca gcccgggctg cgccgttgcg gtttgcgcg gtcgtgtgg tcccgctccg 360  
tgtcgtggca ggtgttctcg tactcgtggt ctactaccc tggatccgcg tggatccgc 420  
gcgggtggag gaggaccggg agggcggcga agggatggg tacgcgcgt tggacgggtg 480  
gaggcgggctg gggctgtgc ggtgcggccg cgcaactcgct cgccatgtgt ttgttgcctt 540  
cggttctat tggatccgag agtacgacag ccgccttccc aatgctgagg atggccatgt 600  
ggaccgtct aaagaaatcg aaaggcctgg ggcaattgtg tctaattatg tatcttatgt 660  
ggatattctt tatcacatgt cagcctctt tcctagttt gttgctaaga gatcagtggc 720  
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ggattatctc ctccattca aaacagggtgc ttttcttgc aaggcaccag ttcaaccagt 960  
catttgaga tatttttaca aaagattaa tgcagcatgg gattccatgt cagggccacg 1020  
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gcatcgcat ggtttagagg aatgtcgta atatactatc cggcataaat ctgtaaagta 1380  
attaccaac tgtcatagtt cagtaattat gttggttata ctcctacatg gttggccatc 1440  
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aa 1502

<210> 46

<211> 395

<212> PRT

<213> Zea mays

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   20               25   30  
  
 Pro Leu Leu Ser Ser Ser Pro Ser Pro Ser Pro Ser Ala Ala Pro  
   35               40   45  
  
 Val Leu Glu Ser Ile Glu Glu Leu Asp Arg Lys Tyr Ala Pro Tyr Ala  
   50               55   60  
  
 Arg Arg Asp Ala Tyr Gly Pro Met Gly Leu Gly Pro Val Ser Ala Ala  
   65               70   80  
  
 Glu Ala Ala Arg Leu Ala Phe Ala Ala Val Val Leu Val Pro Leu Arg  
   85               90   95  
  
 Val Val Ala Gly Val Leu Val Leu Val Val Tyr Tyr Leu Val Cys Arg  
   100              105                                   110  
  
 Val Cys Thr Leu Arg Val Glu Glu Asp Arg Glu Gly Gly Glu Gly Asp  
   115              120                                   125  
  
 Gly Tyr Ala Arg Leu Asp Gly Trp Arg Arg Ala Gly Ala Val Arg Cys  
   130              135                                   140  
  
 Gly Arg Ala Leu Ala Arg Ala Met Leu Phe Val Phe Gly Phe Tyr Trp  
   145              150                                   155                   160  
  
 Ile Arg Glu Tyr Asp Ser Arg Leu Pro Asn Ala Glu Asp Gly His Val  
   165              170                                   175  
  
 Asp Gln Ser Lys Glu Ile Glu Arg Pro Gly Ala Ile Val Ser Asn His  
   180              185                                   190  
  
 Val Ser Tyr Val Asp Ile Leu Tyr His Met Ser Ala Ser Phe Pro Ser  
   195              -- 200                                   205  
  
 Phe Val Ala Lys Arg Ser Val Ala Arg Leu Pro Leu Val Gly Leu Ile  
   210              215                                   220  
  
 Ser Lys Cys Leu Gly Cys Ile Phe Val Gln Arg Glu Ser Lys Thr Pro  
   225              230                                   235                   240  
  
 Asp Phe Lys Gly Val Ser Gly Ala Val Ser Glu Arg Ile His Arg Ala  
   245              250                                   255  
  
 His Gln Gln Lys Asn Ala Pro Met Met Leu Leu Phe Pro Glu Gly Thr  
   260              265                                   270  
  
 Thr Thr Asn Gly Asp Tyr Leu Leu Pro Phe Lys Thr Gly Ala Phe Leu  
   275              280                                   285  
  
 Ala Lys Ala Pro Val Gln Pro Val Ile Leu Arg Tyr Pro Tyr Lys Arg  
   290              295                                   300  
  
 Phe Asn Ala Ala Trp Asp Ser Met Ser Gly Ala Arg His Val Phe Leu  
   305              310                                   315                   320

Leu Leu Cys Gln Phe Val Asn Tyr Leu Glu Val Val Arg Leu Pro Val  
325 330 335

Tyr Tyr Pro Ser Glu Gln Glu Lys Asp Asp Pro Lys Leu Tyr Ala Asn  
340 345 350

Asn Val Arg Lys Leu Met Ala Val Glu Gly Asn Leu Ile Leu Ser Asp  
355 360 365

Leu Gly Leu Ala Glu Lys Arg Val Tyr His Ala Ala Leu Asn Gly Asn  
370 375 380

Ser Leu Ala Arg Ala Leu His Gln Lys Asp Asp  
385 390 395

<210> 47

<211> 1555

<212> DNA

<213> Oryza sativa

<400> 47

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ccctccgacc ccgacgacccct cggcgccggc ggcgaggagg aggaggagag gctcgccctcg 180  
aagccgctgc tctcgtcccc gtccacctat cttccgcgg ggacggagga gggcggtcgag 240  
gagctggagc tcgaccggag gtacgcgccc tacgcgagggc gggacgcgtta cggggcgatg 300  
ggccggggcc ccctggggcg ggcggggccgg gggcggtcg gggtggcgcc cgccgtgctc 360  
ttcccgctcc ggctcgccgc gggcggtcg tcgtcgatcg cctactaccc tctgtggccgc 420  
gtgtgcacgc tgctgttgaa ggaggaggag cgcgagggtg gcgggtggcg ccggctggaa 480  
gaagtggagg gggacgggta cgccgcggc tacgcgatggc gaggggttgg ggcgtgaggg cgtcgatcg 540  
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taegactgcc gctccctga tgctgaggat gagcatcagg aacagtccaa agaattggaa 660  
agaccagggg cagtagtatac taatcatgtt tcttatgtgg atattctta ccacatgtca 720  
tcttccttcc caagctttgt tgccaaagaga tcagtgccca gattgccat ggttgtctc 780  
ataagcaaat gtcttgatg cattttgtt cagcggaaat ctaaaacctc agatttcaaa 840  
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caatttgtaa ataacattga ggtgatccat ttgcctgtgtt attaccatc tgagcaagag 1140  
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<210> 48

<211> 404

<212> PRT

<213> Oryza sativa

<400> 48

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20 25 30

Pro Leu Leu Ser Ser Pro Ser Thr Tyr Pro Ser Ala Gly Thr Glu Glu  
                   35                  40                  45  
  
 Gly Val Glu Glu Leu Glu Leu Asp Arg Arg Tyr Ala Pro Tyr Ala Arg  
                   50                  55                  60  
  
 Arg Asp Ala Tyr Gly Ala Met Gly Arg Gly Pro Leu Gly Ala Ala Gly  
                   65                  70                  75                  80  
  
 Ala Gly Arg Leu Ala Val Gly Ala Ala Val Leu Phe Pro Leu Arg Leu  
                   85                  90                  95  
  
 Ala Ala Gly Val Leu Val Leu Val Ala Tyr Tyr Leu Val Cys Arg Val  
                   100                105                110  
  
 Cys Thr Leu Arg Val Glu Glu Glu Glu Arg Gly Gly Gly Gly Gly  
                   115                120                125  
  
 Ala Ala Gly Glu Val Glu Gly Asp Gly Tyr Ala Arg Leu Glu Gly Trp  
                   130                135                140  
  
 Arg Arg Glu Gly Val Val Arg Cys Gly Arg Ala Leu Ala Arg Ala Met  
                   145                150                155                160  
  
 Leu Phe Val Phe Gly Phe Tyr Trp Ile Arg Glu Tyr Asp Cys Arg Phe  
                   165                170                175  
  
 Pro Asp Ala Glu Asp Glu His Gln Glu Gln Ser Lys Glu Leu Gly Arg  
                   180                185                190  
  
 Pro Gly Ala Val Val Ser Asn His Val Ser Tyr Val Asp Ile Leu Tyr  
                   195                200                205  
  
 His Met Ser Ser Ser Phe Pro Ser Phe Val Ala Lys Arg Ser Val Ala  
                   210                215                220  
  
 Arg Leu Pro Met Val Gly Leu Ile Ser Lys Cys Leu Gly Cys Ile Phe  
                   225                230                235                240  
  
 Val Gln Arg Glu Ser Lys Thr Ser Asp Phe Lys Gly Val Ser Gly Ala  
                   245                250                255  
  
 Val Thr Glu Arg Ile Gln Arg Ala His Gln Gln Lys Asn Ser Pro Met  
                   260                265                270  
  
 Met Leu Leu Phe Pro Glu Gly Thr Thr Asn Gly Asp Tyr Leu Leu  
                   275                280                285  
  
 Pro Phe Lys Thr Gly Ala Phe Leu Ala Lys Ala Pro Val Lys Pro Val  
                   290                295                300  
  
 Ile Leu Arg Tyr Pro Tyr Lys Arg Phe Ser Pro Ala Trp Asp Ser Met  
                   305                310                315                320  
  
 Ser Gly Ala Arg His Val Phe Leu Leu Leu Cys Gln Phe Val Asn Asn  
                   325                330                335  
  
 Leu Glu Val Ile His Leu Pro Val Tyr Tyr Pro Ser Glu Gln Glu Lys  
                   340                345                350

Glu Asp Pro Lys Leu Tyr Ala Asn Asn Val Arg Lys Leu Met Ala Val  
355 360 365

Glu Gly Asn Leu Ile Leu Ser Asp Leu Gly Leu Ala Glu Lys Arg Val  
370 375 380

Tyr His Ala Ala Leu Asn Gly Asn Asn Ser Leu Pro Arg Ala Leu His  
385 390 395 400

Gln Lys Asp Asp

<210> 49

<211> 1072

<212> DNA

<213> Glycine max

<400> 49

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actctgcctc tcaggaagac cgagtcagc ctgaagagtt ggggagaccc agcgtaataa 180  
tatctaatac ttgttcatac ttggatattt tgtatcacat gtcgtcctca ttcccaagtt 240  
ttgttgctaa gagatcagtg gctaaacttc cgctcattgg tctcatcagc aagtgcctt 300  
gttgtgtgt ttttcagcgg gaatcaaagt catcgactt caagggtgtt tcagctgtt 360  
tcactgacag aattcaagaa gtcatcaga atgagtctgc tccattaatg atgttatttc 420  
cagaaggaac aaccacaaat ggagagttcc tccttccatt caagactggt gttttttgg 480  
caaaggcacc agtacttcct gtgattttaa gatatcatta ccagagattt agccccgcct 540  
gggattccat atctgggtt cccatgtaa tatttctcct gtgtcagttt gtgaattata 600  
tggaggtgat ccgagtacct gttaccatc cctcacagca ggagatgaat gatcccaaac 660  
tatatgctaa taatgttaga agttgtatgg ctactgaggg taatttata ctttctgata 720  
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gggtatagct aaatagtata cattcaccta aacatctgaa tggtaattgt gtaattttct 960  
tgtaaataac gtgaccaata atgttttaat tgctggtgaa ctcatttga ggcacacaaat 1020  
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<210> 50

<211> 267

<212> PRT

<213> Glycine max

<400> 50

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20 25 30

Phe Tyr Trp Ile Pro Glu Ser Asn Ser Ala Ser Gln Glu Asp Arg Ser  
35 40 45

Gln Pro Glu Glu Leu Gly Arg Pro Ser Val Ile Ile Ser Asn His Val  
50 55 60

Ser Tyr Leu Asp Ile Leu Tyr His Met Ser Ser Ser Phe Pro Ser Phe  
65 70 75 80

Val Ala Lys Arg Ser Val Ala Lys Leu Pro Leu Ile Gly Leu Ile Ser  
                   85                         90                         95  
  
 Lys Cys Leu Gly Cys Val Tyr Val Gln Arg Glu Ser Lys Ser Ser Asp  
                   100                     105                     110  
  
 Phe Lys Gly Val Ser Ala Val Val Thr Asp Arg Ile Gln Glu Ala His  
                   115                     120                     125  
  
 Gln Asn Glu Ser Ala Pro Leu Met Met Leu Phe Pro Glu Gly Thr Thr  
                   130                     135                     140  
  
 Thr Asn Gly Glu Phe Leu Leu Pro Phe Lys Thr Gly Gly Phe Leu Ala  
                   145                     150                     155                 160  
  
 Lys Ala Pro Val Leu Pro Val Ile Leu Arg Tyr His Tyr Gln Arg Phe  
                   165                     170                     175  
  
 Ser Pro Ala Trp Asp Ser Ile Ser Gly Val Arg His Val Ile Phe Leu  
                   180                     185                     190  
  
 Leu Cys Gln Phe Val Asn Tyr Met Glu Val Ile Arg Val Pro Val Tyr  
                   195                     200                     205  
  
 His Pro Ser Gln Gln Glu Met Asn Asp Pro Lys Leu Tyr Ala Asn Asn  
                   210                     215                     220  
  
 Val Arg Arg Leu Met Ala Thr Glu Gly Asn Leu Ile Leu Ser Asp Ile  
                   225                     230                     235                 240  
  
 Gly Leu Ala Glu Lys Arg Ile Tyr His Ala Ala Leu Asn Gly Asn Asn  
                   245                     250                     255  
  
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 <211> 838  
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 <213> Glycine max  
  
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 <222> (205)  
 <223> n = a, c, g, or t  
  
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 <223> n = a, c, g, or t  
  
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 ctcttgcaat agatccctc gagtactatt atttcccgag ggaacaacaa caaatggcag 180

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gaaccttatac tccttccaac ttggngcatt tatccctgga taccuaatcc agcctgtaat 240
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tatgttcaga atgttcactc aatttcacaa ctttttgag gttagaatatc ttccgtcat 360
ttatcccctg gatgataagg aaactgctgt acattttcg  gagaggacta gccgtgctat 420
cgcaactgca ctaaatgctg tccagacagg acattctt  ggagacataa tgcttcata 480
gaaagcacaa gaagcaaaac aggagaaccc ctcaagttt atggttgaaa tgaccaaggt 540
ggaatcagtg agtccctaaa agcaaatgac cttaccattt ccttttttt tctgccattt 600
tcaagtccct tgtaaattat cttttctt aactttt  gtaggatatt taggttaaac 660
cttttgaagt acatgcaaat gccacagtaa cccttgctt atgccaatgg atgacagaca 720
taagtgaccc agggtggtc  cataatgtt  gggccttcta atctatgg  aatatgtant 780
gaaaggggag aatatttaaa ttgtgattt  tggnaataag gggataatat gacataag 838

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<210> 52  
<211> 185  
<212> PRT  
<213> Glycine max

<400> 52  
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 Gln Val Ile Tyr Val Asn Arg Phe Leu Pro Ser Ser Arg Lys Gln Ala  
 20 25 30  
 Val Arg Glu Ile Lys Arg Arg Ala Ser Cys Asn Arg Phe Pro Arg Val  
 35 40 45  
 Leu Leu Phe Pro Glu Gly Thr Thr Asn Gly Arg Asn Leu Ile Ser  
 50 55 60  
 Phe Gln Leu Gly Ala Phe Ile Pro Gly Tyr Pro Ile Gln Pro Val Ile  
 65 70 75 80  
 Val Arg Tyr Pro His Val His Phe Asp Gln Ser Trp Gly His Val Ser  
 85 90 95  
 Leu Gly Lys Leu Met Phe Arg Met Phe Thr Gln Phe His Asn Phe Phe  
 100 105 110  
 Glu Val Glu Tyr Leu Pro Val Ile Tyr Pro Leu Asp Asp Lys Glu Thr  
 115 120 125  
 Ala Val His Phe Arg Glu Arg Thr Ser Arg Ala Ile Ala Thr Ala Leu  
 130 135 140  
 Asn Ala Val Gln Thr Gly His Ser Tyr Gly Asp Ile Met Leu His Met  
 145 150 155 160  
 Lys Ala Gln Glu Ala Lys Gln Glu Asn Pro Ser Ser Phe Met Val Glu  
 165 170 175  
 Met Thr Lys Val Glu Ser Val Ser Pro  
 180 185

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<210> 53
<211> 1632
<212> DNA
<213> Oryza sativa
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<400> 53

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 cccactcgatc ctcgtcgatc tcccgctcg tccctcttc ctcctctccg gcctcatcat 240  
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 ttagcatgca cttgtcatat caaataatcg gagcgatatac gattggctta ttgggtggat 480  
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 agccaaggcg gctcgaaacc gtgtcaagaa agattgaaag agatgaagat agagtctgca 1320  
 gcttatcaat gggagctacc aattaattgg gtattgaatt catgtaggca aaaaaattga 1380  
 gggcctaatac tttcctgtat aatgcaccaa aagggttctt acagaactga atgcctgaat 1440  
 agagagattc taggagattt ggtgaactag caactctgag ctctgttgc ctgtattttc 1500  
 agagaatgtt tttttggca gaacaggaat tgtactactt gtatttatttgaacttctac 1560  
 atcagtctgg atttggatc aagacctta gtgatttgc tatcagtgaa acttaaaaaaa 1620  
 aaaaaaaaaaa aa 1632

<210> 54  
 <211> 374  
 <212> PRT  
 <213> Oryza sativa

<400> 54

Met	Ala	Val	Pro	Leu	Val	Leu	Val	Val	Leu	Pro	Leu	Gly	Leu	Leu	Phe
1									10						15

  

Leu	Leu	Ser	Gly	Leu	Ile	Ile	Asn	Ala	Ile	Gln	Ala	Val	Leu	Phe	Leu
									25						30

  

Ser	Ile	Arg	Pro	Phe	Ser	Lys	Ser	Leu	Tyr	Arg	Arg	Ile	Asn	Arg	Phe
								35				40		45	

  

Leu	Ala	Glu	Leu	Leu	Trp	Leu	Gln	Leu	Val	Trp	Leu	Val	Asp	Trp	Trp
								50			55		60		

  

Ala	Gly	Val	Lys	Ile	Gln	Leu	His	Ala	Asp	Asp	Glu	Thr	Tyr	Lys	Ala
								65			70		75		80

  

Met	Gly	Asn	Glu	His	Ala	Leu	Val	Ile	Ser	Asn	Asn	Arg	Ser	Asp	Ile
								85				90		95	

  

Asp	Trp	Leu	Ile	Gly	Trp	Ile	Leu	Ala	Gln	Arg	Ser	Gly	Cys	Leu	Gly
								100			105		110		

  

Ser	Thr	Leu	Ala	Val	Met	Lys	Lys	Ser	Ser	Lys	Phe	Leu	Pro	Val	Ile
								115			120		125		

Gly Trp Ser Met Trp Phe Ala Glu Tyr Leu Phe Leu Glu Arg Ser Trp  
130 135 140

Ala Lys Asp Glu Lys Thr Leu Lys Trp Gly Leu Gln Arg Leu Lys Asp  
145 150 155 160

Phe Pro Arg Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe  
165 170 175

Thr Pro Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Val Ser Gln Gly  
180 185 190

Leu Pro Ala Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val  
195 200 205

Ser Ala Val Thr Ile Met Arg Asp Phe Val Pro Ala Ile Tyr Asp Thr  
210 215 220

Thr Val Ile Ile Pro Lys Asp Ser Pro Gln Pro Thr Met Leu Arg Ile  
225 230 235 240

Leu Lys Gly Gln Ser Ser Val Val His Val Arg Met Lys Arg His Ala  
245 250 255

Met Ser Glu Met Pro Lys Ser Glu Asp Asp Val Ser Lys Trp Cys Lys  
260 265 270

Asp Ile Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Leu Ala Thr  
275 280 285

Gly Thr Phe Asp Glu Glu Ile Arg Pro Ile Gly Arg Pro Val Lys Ser  
290 295 300

Leu Leu Val Thr Leu Phe Trp Ser Cys Leu Leu Leu Tyr Gly Ala Val  
305 310 315 320

Lys Leu Phe Leu Trp Thr Gln Leu Leu Ser Thr Trp Lys Gly Val Gly  
325 330 335

Phe Thr Gly Leu Gly Leu Ala Leu Val Thr Ala Val Met His Val Phe  
340 345 350

Ile Met Phe Ser Gln Ser Glu Arg Ser Ser Ser Ala Lys Ala Ala Arg  
355 360 365

Asn Arg Val Lys Lys Asp  
370

<210> 55

<211> 1498

<212> DNA

<213> Glycine max

<400> 55

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tggcatgc tattgcagca gcccgtgg tggtaccatt gggcctgctc ttcttcgcct 180  
ccggcctcct tggtaatctc attcaggcaa tatgctatgt cgtcgttaagg ccgggtgtcga 240  
aaagtttcta cagaaggatc aaccgggttag tagcagagct cttgtggctg gagcttgtat 300  
ggcttattga ttggtgggca ggagttaagg tccaaatatt cacagatcat gaaacccattc 360

gttaatggg taaagagcat gcacttgtga taagcaatca cagaagtat attgattggc 420  
 ttgttggatg ggttcagct cagcgttcag gttgtcttgg cagcactcta gctgtatga 480  
 agaaaatctc aaagttctg ccggtcattg gctggtcaat gtggtttct gagtatctt 540  
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 gtgatttccc tcttcctt tggctagtc tctttgtaga aggaacgcgt tttacacagg 660  
 ccaaactatt agctgctcag gaatatgccca cttccactgg attgcctgtt cctagaaaatg 720  
 tttgattcc aagaactaag gttttgtt ctgcagtaag tcataatgcgc tcatttgc 780  
 ctgccattt tgatgtaca gtagccatcc ctaagagttc ccctgctcct acaatgctaa 840  
 gactctcaa gggacaaacct tcagtggtgc atgttcatat caagaggcat ttgatgaagg 900  
 aactgccaga tacagatgag gctgttgc aatgggtcg agatatattt gtggccaagg 960  
 atgcttgtt agacaaacat atggctgagg gtacttttag tgatcaagag ctgcaggata 1020  
 ctggtcgacc aataaagtct cttctggtag ttatatctt ggcgtgtctg gttgttgcgg 1080  
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 cttatcgatt cattgtttt aatttaatta ggatattcctt ttgttattgac agtcttaggg 1440  
 atggctaga aaaattcaac cacctatttt attttaaaaa aaaaaaaaaa aaaaaact 1498

<210> 56

<211> 377

<212> PRT

<213> Glycine max

<400> 56

Met	Ala	Ile	Ala	Ala	Ala	Val	Val	Val	Pro	Leu	Gly	Leu	Leu	Phe
1									10					15

Phe	Ala	Ser	Gly	Leu	Leu	Val	Asn	Leu	Ile	Gln	Ala	Ile	Cys	Tyr	Val
				20				25					30		

Val	Val	Arg	Pro	Val	Ser	Lys	Ser	Leu	Tyr	Arg	Arg	Ile	Asn	Arg	Val
						35		40				45			

Val	Ala	Glu	Leu	Leu	Trp	Leu	Glu	Leu	Val	Trp	Leu	Ile	Asp	Trp	Trp
					50				55			60			

Ala	Gly	Val	Lys	Val	Gln	Ile	Phe	Thr	Asp	His	Glu	Thr	Phe	Arg	Leu
					65			70		75			80		

Met	Gly	Lys	Glu	His	Ala	Leu	Val	Ile	Ser	Asn	His	Arg	Ser	Asp	Ile
								85		90			95		

Asp	Trp	Leu	Val	Gly	Trp	Val	Ser	Ala	Gln	Arg	Ser	Gly	Cys	Leu	Gly
					100				105			110			

Ser	Thr	Leu	Ala	Val	Met	Lys	Lys	Ser	Ser	Lys	Phe	Leu	Pro	Val	Ile
					115				120			125			

Gly	Trp	Ser	Met	Trp	Phe	Ser	Glu	Tyr	Leu	Phe	Leu	Glu	Arg	Ser	Trp
					130			135			140				

Ala	Lys	Asp	Glu	Ser	Thr	Leu	Lys	Ser	Gly	Ile	Gln	Arg	Leu	Ser	Asp
						145		150		155		160			

Phe	Pro	Leu	Pro	Phe	Trp	Leu	Ala	Leu	Phe	Val	Glu	Gly	Thr	Arg	Phe
								165		170			175		

Thr Gln Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Thr Ser Thr Gly  
 180 185 190  
 Leu Pro Val Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val  
 195 200 205  
 Ser Ala Val Ser His Met Arg Ser Phe Val Pro Ala Ile Tyr Asp Val  
 210 215 220  
 Thr Val Ala Ile Pro Lys Ser Ser Pro Ala Pro Thr Met Leu Arg Leu  
 225 230 235 240  
 Phe Lys Gly Gln Pro Ser Val Val His Val His Ile Lys Arg His Leu  
 245 250 255  
 Met Lys Glu Leu Pro Asp Thr Asp Glu Ala Val Ala Gln Trp Cys Arg  
 260 265 270  
 Asp Ile Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Met Ala Glu  
 275 280 285  
 Gly Thr Phe Ser Asp Gln Glu Leu Gln Asp Thr Gly Arg Pro Ile Lys  
 290 295 300  
 Ser Leu Leu Val Val Ile Ser Trp Ala Cys Leu Val Val Ala Gly Ser  
 305 310 315 320  
 Val Lys Phe Leu Gln Trp Ser Ser Leu Leu Ser Ser Trp Lys Gly Val  
 325 330 335  
 Ala Phe Ser Ala Phe Gly Leu Ala Val Val Thr Ala Leu Met Gln Ile  
 340 345 350  
 Leu Ile Gln Phe Ser Gln Ser Glu Arg Ser Asn Pro Ala Lys Ile Val  
 355 360 365  
 Pro Ala Lys Ser Lys Asn Lys Gly Ser  
 370 375

<210> 57  
 <211> 1415  
 <212> DNA  
 <213> Triticum aestivum

<400> 57  
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 tcttgcgtat aaggccattc tcgaagcgat tgtaccggca gatcaacgta ttcctggccg 180  
 agttgttgtg gcttcagctg atctggcttg tggactggtg ggcaggtatt aaggtacagg 240  
 tgtatgcgga tccagaaaact tgaaaactaa tggcaaaaga gcacgccctt ctcataatcca 300  
 atcatcgaag tgacattgtat tggctgggtt gatggatttt agcacagcgt tcaggatgtc 360  
 ttgaaagcgc aatacgatata atgaaaaat cctcaaagtt cttccagtt attgggttgt 420  
 ccatgtgggtt tgcagaatac ctcttttgg agagaagctg ggcaaaaggat gaaaaaacac 480  
 ttaaatcggg tcttcaaagg ttgaaaagact tccccagatc attttggctt gcccttttg 540  
 ttgagggtac aagatttact ccagaaaaac ttttagcagc tcaagaatat gcagtctcac 600  
 agggtttgcg agcgcctagg aatgtgctga ttccacgaac aaaggattt gtatcagctg 660  
 taagtattat gcgtgacttt gtcccagcta tctacgatac aacagtgatt attccggaaag 720  
 attcgcttaa accaacaatg ctgcgtattc ttcagggaca atcatcagtt gttcatgtcc 780  
 gcataaaaacg ccattcaatg agtgatatgc ctaactcgga tgaggatgtt tcaaaatggt 840  
 gcaaaagatat attttagca aaggacgcgt tattggacaa acatatacgca actggtaactt 900

ttgatgagga aattatacca attggccgtc cagtcaaatac tttgatggtg gtcctgtctt 960  
ggcatgtct cctcctataat ggtgctcata gattcttaca gtggaccagg ctcttgcga 1020  
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tgaagaaggat ttgatagctc gtgtgaaatt cagtctatag gggactgcc aatttattat 1200  
gttcagaata tatgttagaca caggctccat gggtaaccatc tagtatgtcc ttgttgcct 1260  
cggttaagagc tttaggaaatt ttgtgtggcg agaactgtga gctttcttcc ttctttctct 1320  
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cgaagctttt ttttatcaaa aaaaaaaaaaaa aaaaaa 1415

<210> 58  
<211> 374  
<212> PRT  
<213> Triticum aestivum

<400> 58  
Met Ala Ile Pro Leu Val Val Leu Leu Pro Leu Gly Leu Leu Phe  
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Leu Leu Ser Gly Leu Val Val Asn Thr Val Gln Ala Val Leu Phe Leu  
20 25 30  
  
Thr Ile Arg Pro Phe Ser Lys Arg Leu Tyr Arg Gln Ile Asn Val Phe  
35 40 45  
  
Leu Ala Glu Leu Leu Trp Leu Gln Leu Ile Trp Leu Val Asp Trp Trp  
50 55 60  
  
Ala Gly Ile Lys Val Gln Val Tyr Ala Asp Pro Glu Thr Trp Lys Leu  
65 70 75 80  
  
Met Gly Lys Glu His Ala Leu Leu Ile Ser Asn His Arg Ser Asp Ile  
85 90 95  
  
Asp Trp Leu Val Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly  
100 105 110  
  
Ser Ala Ile Ala Ile Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile  
115 120 125  
  
Gly Trp Ser Met Trp Phe Ala Glu Tyr Leu Phe Leu Glu Arg Ser Trp  
130 135 140  
  
Ala Lys Asp Glu Lys Thr Leu Lys Ser Gly Leu Gln Arg Leu Lys Asp  
145 150 155 160  
  
Phe Pro Arg Ser Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe  
165 170 175  
  
Thr Pro Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Val Ser Gln Gly  
180 185 190  
  
Leu Thr Ala Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val  
195 200 205  
  
Ser Ala Val Ser Ile Met Arg Asp Phe Val Pro Ala Ile Tyr Asp Thr  
210 215 220  
  
Thr Val Ile Ile Pro Glu Asp Ser Pro Lys Pro Thr Met Leu Arg Ile  
225 230 235 240

Leu Gln Gly Gln Ser Ser Val Val His Val Arg Ile Lys Arg His Ser  
245 250 255

Met Ser Asp Met Pro Asn Ser Asp Glu Asp Val Ser Lys Trp Cys Lys  
260 265 270

Asp Ile Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Ile Ala Thr  
275 280 285

Gly Thr Phe Asp Glu Glu Ile Ile Pro Ile Gly Arg Pro Val Lys Ser  
290 295 300

Leu Met Val Val Leu Ser Trp Ser Cys Leu Leu Tyr Gly Ala His  
305 310 315 320

Arg Phe Leu Gln Trp Thr Gln Leu Leu Ser Thr Trp Lys Gly Val Ile  
325 330 335

Leu Phe Ala Ser Gly Leu Ala Met Val Thr Ala Val Met His Val Phe  
340 345 350

Ile Met Phe Ser Gln Ala Glu Arg Ser Ser Ser Ala Lys Ala Ala Arg  
355 360 365

Asp Arg Val Lys Lys Asp  
370